

L Number	Hits	Search Text	DB	Time stamp
1	6	vogeli-gabriel.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/12/02 07:29
2	20	lind-peter.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/12/02 07:29
3	12	parodi-luis-a.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/12/02 07:30
4	3	wood-linda-s.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/12/02 07:30
5	2	hiebsch-ronald-r.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/12/02 07:30
6	3085	g adj protein adj coupled adj receptor	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/12/02 07:31
7	1174	(g adj protein adj coupled adj receptor) same human	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/12/02 07:32

09714449 Results

SEQ ID NO: 85

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1020	100.0	1020	6	AX147840	AX147840 Sequence
2	980.8	96.2	1081	6	AX458238	AX458238 Sequence
3	980.8	96.2	1092	9	AF370886	AF370886 Homo sapi
4	980.8	96.2	1414	9	AB065877	AB065877 Homo sapi
5	980.8	96.2	9905	6	AX379470	AX379470 Sequence
c 6	980.8	96.2	67645	9	AL356486	AL356486 Human DNA
7	980.8	96.2	156555	9	AC026756	AC026756 Homo sapi
8	979.2	96.0	1729	6	AX191332	AX191332 Sequence
9	977.8	95.9	1014	6	AX148186	AX148186 Sequence
10	977.8	95.9	1014	6	AX379468	AX379468 Sequence
11	977.8	95.9	1014	6	AX384211	AX384211 Sequence
12	977.8	95.9	1014	9	AB083598	AB083598 Homo sapi
13	977.8	95.9	1014	9	AF411109	AF411109 Homo sapi
14	976.2	95.7	1014	6	AX305130	AX305130 Sequence
15	976.2	95.7	1014	6	AX464561	AX464561 Sequence
c 16	701.4	68.8	202838	2	AC108794	AC108794 Mus muscu
c 17	578	56.7	578	6	AX147814	AX147814 Sequence
18	335	32.8	2245	6	AX384210	AX384210 Sequence

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1020	100.0	1020	22	AAH51011	Human nGPCR54 codi
2	980.8	96.2	1288	24	ABL56197	Human P2Y1-li enco
3	980.8	96.2	5435	24	ABL56198	Human P2Y1-li enco
4	980.8	96.2	9905	24	AAK98324	Human purinergic-r
5	979.2	96.0	1729	22	AAS08362	Human cDNA encodin
6	979.2	96.0	1729	23	ABV24026	Human prostate exp
7	979.2	96.0	1729	23	ABV25767	Human prostate exp
8	979.2	96.0	1729	23	ABV29909	Human prostate exp
9	979.2	96.0	1729	23	ABV30024	Human prostate exp
10	977.8	95.9	1014	22	AAS07948	Human cDNA encodin
11	977.8	95.9	1014	24	ABN85630	Human P2Y-like rec
12	977.8	95.9	1014	24	ABK11381	Human DNA encoding
13	977.8	95.9	1014	24	AAK98323	Human purinergic-r
14	976.2	95.7	1014	24	ABQ78847	Human G-protein co
15	976.2	95.7	1014	24	AAD34278	Human AXOR89 (G-pr
16	976.2	95.7	1014	24	AAD26370	Human G-protein co
17	974.8	95.6	1011	24	AAL43942	Human G protein-co
18	794.8	77.9	831	24	ABN85629	Human P2Y-like rec
19	726.2	71.2	1313	22	AAK52430	Human polynucleoti
c 20	578	56.7	578	22	AAH50998	Human nGPCR54 codi
c 21	562.8	55.2	740	23	ABV15662	Human prostate exp
c 22	476.6	46.7	545	22	ABA08326	Human P2Y purinoce
c 23	476.6	46.7	545	22	AAK53414	Human polynucleoti
c 24	426.2	41.8	539	23	ABV39127	Human prostate exp

RESULT 1

AAH51011

ID AAH51011 standard; DNA; 1020 BP.

XX

AC AAH51011;

XX

DT 28-AUG-2001 (first entry)

XX

DE Human nGPCR54 coding sequence #2.

XX

KW G protein-coupled receptor; nGPCR; seven transmembrane receptor;

KW signal transduction; schizophrenia; thyroid disorder; renal failure;
 KW rheumatoid arthritis; CNS disorder; infection; metabolic disease;
 KW cardiovascular disease; proliferative disorder; hormonal disorder;
 KW neurological disorder; neuronal disorder; Alzheimer's disease; cancer;
 KW attention deficit-hyperactivity disorder/attention deficit disorder;
 KW Parkinson's disease; migraine; senile dementia; inflammatory disease;
 KW rheumatoid arthritis; autoimmune disorder; respiratory ailment;
 KW neuroprotective; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200136473-A2.
 XX
 PD 25-MAY-2001.
 XX
 PF 16-NOV-2000; 2000WO-US31581.
 XX
 PR 16-NOV-1999; 99US-0165838.
 PR 17-NOV-1999; 99US-0166071.
 PR 19-NOV-1999; 99US-0166678.
 PR 28-DEC-1999; 99US-0173396.
 PR 22-FEB-2000; 2000US-0184129.
 PR 28-FEB-2000; 2000US-0185421.
 PR 28-FEB-2000; 2000US-0185554.
 PR 02-MAR-2000; 2000US-0186530.
 PR 03-MAR-2000; 2000US-0186811.
 PR 09-MAR-2000; 2000US-0188114.
 PR 17-MAR-2000; 2000US-0190310.
 PR 21-MAR-2000; 2000US-0190800.
 PR 20-APR-2000; 2000US-0198568.
 PR 02-MAY-2000; 2000US-0201190.
 PR 08-MAY-2000; 2000US-0203111.
 PR 25-MAY-2000; 2000US-0207094.
 XX
 PA (PHAA) PHARMACIA & UPJOHN CO.
 XX
 PI Vogeli G, Wood LS, Parodi LA, Hiebsch RR, Lind P, Slightom J;
 PI Schellin KA, Kaytes PS, Bannigan CM, Ruff V, Sejlitz T, Huff RM;
 XX
 DR WPI; 2001-389826/41.
 DR P-PSDB; AAG80971.
 XX
 PT New G protein-coupled receptor (nGPCR-x) and its encoding
 PT polynucleotide useful for diagnosing and treating e.g. schizophrenia -
 XX
 PS Claim 4; Page 91; 261pp; English.
 XX
 CC The present invention relates to novel G protein-coupled receptors
 CC (nGPCRx; where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27,
 CC 28, 31-38, 40, 41, 53-60) and their coding sequences. The present
 CC sequence is the coding sequence for one such G protein-coupled receptor.
 CC GPCRs are also known as seven transmembrane receptors and function in
 CC signal transduction. The nGPCRx coding sequences are useful for
 CC screening a human to diagnose a disorder affecting the brain or a genetic
 CC predisposition, specifically schizophrenia. nGPCRx are useful for
 CC identifying compounds useful for treating schizophrenia. Detection of
 CC nGPCRx in a sample is useful as a diagnostic tool for diseases or
 CC disorders e.g. thyroid disorders, renal failure, rheumatoid arthritis,
 CC CNS disorders, infections such as HIV-1, metabolic and cardiovascular
 CC diseases, proliferative disorders and hormonal disorders. Modulators of
 CC nGPCRx activity have the utility for treating neurological disorders,
 CC including schizophrenia, ADHD/ADD (attention deficit-hyperactivity
 CC disorder/attention deficit disorder), and neuronal disorders such as
 CC Alzheimer's disease, Parkinson's disease, migraine and senile dementia.
 CC Additional disorders include inflammatory conditions (e.g. Crohn's
 CC disease), rheumatoid arthritis, autoimmune disorders, cancers,
 CC respiratory ailments such as asthma, and inflammatory diseases e.g.
 CC inflammatory bowel disease.
 XX
 SQ Sequence 1020 BP; 261 A; 263 C; 190 G; 306 T; 0 other;

Query Match 100.0%; Score 1020; DB 22; Length 1020;
Best Local Similarity 100.0%; Pred. No. 3.3e-287;
Matches 1020; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 ACCATGAATGAGCCACTAGACTATTTAGCAAATGCTTCTGATTTCCTCCGATTATGCAGCT 60
      |||
Db      1 ACCATGAATGAGCCACTAGACTATTTAGCAAATGCTTCTGATTTCCTCCGATTATGCAGCT 60

Qy     61 GCTTTTGAAATTGCACTGATGAAAACATCCCACTCAAGATGCACTACCTCCCTGTTATT 120
      |||
Db     61 GCTTTTGAAATTGCACTGATGAAAACATCCCACTCAAGATGCACTACCTCCCTGTTATT 120

Qy    121 TATGGCATTATCTTCTCGTGGGATTTCCAGGCAATGCAGTAGTGATATCCACTTACATT 180
      |||
Db    121 TATGGCATTATCTTCTCGTGGGATTTCCAGGCAATGCAGTAGTGATATCCACTTACATT 180

Qy    181 TTCAAAATGAGACCTTGGAAGAGCAGCACCATCATTATGCTGAACCTGGCCTGCACAGAT 240
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Db    181 TTCAAAATGAGACCTTGGAAGAGCAGCACCATCATTATGCTGAACCTGGCCTGCACAGAT 240

Qy    241 CTGCTGTATCTGACCAGCCTCCCCTTCTGATTCACTACTATGCCAGTGGCGAAAACCTGG 300
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Db    241 CTGCTGTATCTGACCAGCCTCCCCTTCTGATTCACTACTATGCCAGTGGCGAAAACCTGG 300

Qy    301 ATCTTTGGAGATTTTATGTGTAAGTTTATCCGCTTCAGCTTCCATTTCACCTGTATAGC 360
      |||
Db    301 ATCTTTGGAGATTTTATGTGTAAGTTTATCCGCTTCAGCTTCCATTTCACCTGTATAGC 360

Qy    361 AGCATCTCTTCTCACCTGTTTCAGCATCTTCCGCTACTGTGTGATCATTACCCAATG 420
      |||
Db    361 AGCATCTCTTCTCACCTGTTTCAGCATCTTCCGCTACTGTGTGATCATTACCCAATG 420

Qy    421 AGCTGCTTTTCCATTACAAAACCTCGATGTGAGTTGTAGCCTGTGCTGTGGTGTGGATC 480
      |||
Db    421 AGCTGCTTTTCCATTACAAAACCTCGATGTGAGTTGTAGCCTGTGCTGTGGTGTGGATC 480

Qy    481 ATTTCACTGGTAGCTGTTCATTCCGATGACCTTCTTGATCACATCAACCAACAGGACCAAC 540
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Db    481 ATTTCACTGGTAGCTGTTCATTCCGATGACCTTCTTGATCACATCAACCAACAGGACCAAC 540

Qy    541 AGATCAGCCTGTCTCGACCTCACCAGTTCGGATGAACTCAATACTATTAAGTGGTACAAC 600
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Db    541 AGATCAGCCTGTCTCGACCTCACCAGTTCGGATGAACTCAATACTATTAAGTGGTACAAC 600

Qy    601 CTGATTTTGACTGCAAGTACTTTCTGCCTCCCCTTGGTGATAGTGACACTTTGCTATACC 660
      |||
Db    601 CTGATTTTGACTGCAAGTACTTTCTGCCTCCCCTTGGTGATAGTGACACTTTGCTATACC 660

Qy    661 ACGATTATCCACACTTTGACCCATGGACTGCAAACCTGACAGCTGCCTTAAGCAGAAAGCA 720
      |||
Db    661 ACGATTATCCACACTTTGACCCATGGACTGCAAACCTGACAGCTGCCTTAAGCAGAAAGCA 720

Qy    721 CGAAGGCTAACCATTCTGCTACTCCTTGCAATTTACGTATGTTTTTACCCTTCCATATC 780
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Db    721 CGAAGGCTAACCATTCTGCTACTCCTTGCAATTTACGTATGTTTTTACCCTTCCATATC 780

Qy    781 TTGAGGGTCATTAGGATCGAATCTCAGCCTGCTTTCAATCAGTTGTTCCATTGAGAATC 840
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Qy    841 AGATCCATGAAGCTTACATCGTTTCTAGACCATTATGCTGCTCTGAACACCTTTGGTAAC 900
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Db    841 AGATCCATGAAGCTTACATCGTTTCTAGACCATTATGCTGCTCTGAACACCTTTGGTAAC 900

Qy    901 CTGTTACTATATGTGGTGGTCAGCGACAACTTTCAGCAGGCTGTCTGCTCAACAGTGAGA 960
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Db    901 CTGTTACTATATGTGGTGGTCAGCGACAACTTTCAGCAGGCTGTCTGCTCAACAGTGAGA 960

Qy    961 TGCAAAGTAAGCGGGAACCTTGAGCAAGCAAAGAAAATTAGTTACTCAAACAACCCTTGA 1020
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No.	Score	Match	Length	DB	ID	Description
1	210	20.6	744	14	BM723768	BM723768 UI-E-EO1-
2	126.6	12.4	623	14	BQ038875	BQ038875 pgnlc.pk0
3	115.6	11.3	641	14	BQ396255	BQ396255 NISC_ngl9
4	114.6	11.2	638	9	AL675845	AL675845 AL675845
5	109.4	10.7	877	12	BG402029	BG402029 602466748
6	108.8	10.7	663	13	BM426517	BM426517 pgf2n.pk0
c 7	107.4	10.5	1101	17	CNS0532S	AL318925 Tetraodon
8	106.2	10.4	491	12	BG712193	BG712193 pg1ln.pk0
9	103	10.1	609	9	AL588350	AL588350 AL588350
10	102	10.0	520	9	AI663305	AI663305 uk27c10.y
11	100.4	9.8	2542	11	AK017378	AK017378 Mus muscu
12	100.4	9.8	3001	11	AK005013	AK005013 Mus muscu
13	100	9.8	422	10	BB847918	BB847918 BB847918
14	99.6	9.8	801	13	BG924078	BG924078 602823635
15	98.4	9.6	606	17	AZ953874	AZ953874 2M0219L17
16	97.2	9.5	851	13	BI833118	BI833118 603090834
c 17	95.8	9.4	408	13	BI401676	BI401676 MI-P-CP0-

RESULT 1

BM723768

LOCUS BM723768 744 bp mRNA linear EST 01-MAR-2002

DEFINITION UI-E-EO1-aix-g-16-0-UI.r1 UI-E-EO1 Homo sapiens cDNA clone
UI-E-EO1-aix-g-16-0-UI 5', mRNA sequence.

ACCESSION BM723768

VERSION BM723768.1 GI:19045099

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 744)

AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene
discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)

MEDLINE 97044477

COMMENT Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa

451 Eckstein Medical Research Building Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: msoares@blue.weeg.uiowa.edu

Tissue Procurement: Dr. Gregg Hageman

cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa

DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa

Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).

Seq primer: M13 Reverse.

FEATURES

source

Location/Qualifiers

1..744

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="UI-E-EO1-aix-g-16-0-UI"

/clone_lib="UI-E-EO1"

/tissue_type="fetal eye"

/dev_stage="fetal"

/lab_host="DH10B (Life Technologies) (T1 phage resistant)"

/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-E-EO1 is a normalized cDNA library containing the
following tissue(s): fetal eye. The library was

constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CGCGTATACC. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."

BASE COUNT 217 a 168 c 126 g 233 t
ORIGIN

Query Match 20.6%; Score 210; DB 14; Length 744;
Best Local Similarity 98.8%; Pred. No. 1.8e-51;
Matches 243; Conservative 0; Mismatches 0; Indels 3; Gaps 3;

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Qy   775 CATATCTTGAGGGTCATTCAGGATCGAATCTCAGCCTGCTTTCAATCAGTTGTTCCATTG 834
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Qy   835 AGAATCAGATCCATGAAGCTTACATCGTTTCTAGACCATTATGCTGCTCTGAACACCTTT 894
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Db    59 AGAATCAGATCCATGAAGCTTACATCGTTTCTAGACCATTATGCTGCTCTGAACACCTTT 117

Qy   895 GGTAACCTGTTACTATATGTGGTGGTCAGCGACAACCTTTCAGCAGGCTGTCTGCTCAACA 954
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Db   118 GGTAACCTGTTACTATATGTGGTGGTCAGCGACAACCTTTCAGCAGGCTGTCTGCTCAACA 177

Qy   955 GTGAGATGCAAAGTAAGCGGGAACCTTGAGCAAGCAAAGAAAATTAGTTACTCAAACAAC 1014
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Db   178 GTGAGATGCAAAGTAAGCGGGAACCTTGAGCAAGCAAAGAAAATTAGTTACTCAAACAAC 237

Qy  1015 CCTTGA 1020
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Db   238 CCTTGA 243

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AI663305
LOCUS AI663305 520 bp mRNA linear EST 10-MAY-1999
DEFINITION uk27c10.y1 Sugano mouse kidney mkia Mus musculus cDNA clone
IMAGE:1970226 5' similar to SW:P2YR_RAT P49651 P2Y PURINOCEPTOR 1
; , mRNA sequence.
ACCESSION AI663305
VERSION AI663305.1 GI:4766888
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 520)
AUTHORS Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person
,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter
,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
Waterston,R. and Wilson,R.
TITLE The WashU-NCI Mouse EST Project 1999
JOURNAL Unpublished (1999)
COMMENT Other_ESTs: uk27c10.x1
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:986966

Seq primer: custom primer used

High quality sequence stop: 490.

FEATURES
source Location/Qualifiers
1. .520
/organism="Mus musculus"
/strain="C57BL"
/db_xref="taxon:10090"
/clone="IMAGE:1970226"
/clone_lib="Sugano mouse kidney mkia"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: kidney; Vector: pME18S-FL3; Site_1: DraIII (CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [TGTGGCCTACTGG], digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end primer CGACCTGCAGCTCGAGCACA."

BASE COUNT 127 a 126 c 107 g 160 t
ORIGIN

Query Match 10.0%; Score 102; DB 9; Length 520;
Best Local Similarity 53.4%; Pred. No. 3.3e-19;
Matches 238; Conservative 0; Mismatches 205; Indels 3; Gaps 1;

Qy 62 CTTTGGAAATGCACTGATGAAACATCCCACTCAAGATGCACTACCTCCCTGTTATTT 121
||| || |||| | | | | | | | | | | | |
Db 73 CTTGTGAGAATGGTTGGCAACAGAGGCTATCTGAATAAGTACTACCTCTCTGCATTTT 132

Qy 122 ATGGCATTATCTTCCTCGTGGGATTTCCAGGCAATGCAGTAGTGATATCCACTTACATTT 181
||| || ||| | | ||| | | |||| | | | | | |
Db 133 ATGCAATCGAGTTCATTTTGGACTGCTTGGGAATGTCACTGTGGTGTGGCTACCTCT 192

Qy 182 TCAAAATGAGACCTTGAAGAGCAGCACCATCATTATGCTGAACCTGGCCTGCACAGATC 241
|| |||| |||| |||| | | | | | | | | | |
Db 193 TCTGCATGAAGAACTGGAACAGCAGCAATGTCTATCTTTTAACTTTCCATCTCTGACT 252

Qy 242 TGCTGTATCTGACCAGCCTCCCTTCCTGATTCACTACTATGCCAGTGGCGAAAACCTGGA 301
| | | | | | | | | | | | | | | | | | | |
Db 253 TTGCTTTCCTGTGCACCCTTCCCATCCTGATAAGAGTTATGCCAAT--GATAAGGGGA 309

Qy 302 TCTTTGGAGATTTCATGTGTAAGTTTATCCGCTTCAGCTTCCATTTCAACCTGTATAGCA 361
|| |||| || | | |||| | ||| | | | | | | | |
Db 310 CCTATGGAGATGTTCTCTGTATAAGCAACCGATATGTGCTTACACCAACCTCTACACCA 369

Qy 362 GCATCCTCTTCTCACCTGTTTCAGCATCTTCCGCTACTGTGTGATCATTACCCCAATGA 421
||| |||| |||| | | ||| ||| | | | | | | | |
Db 370 GCATGCTCTTGCTCACTGTCTATTATCATGGACCGATATCTGCTCATGAAGTACCCTGTCC 429

Qy 422 GCTGCTTTTCCATTCAAAAACCTCGATGTGCAGTTGTAGCCTGTGCTGTGGTGTGGATCA 481
| | | | | | | | | | | | | | | | | | | |
Db 430 GAGAACACTTTCTACAAAAGAAGGAATTTGCCATTTTAATCTCGCTGGCTGTCTGGGCCCT 489

Qy 482 TTTCCTGGTAGCTGTCTATTCCGATG 507
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Db 490 TAGTGACCTTAGAAGTTCTACCCATG 515

SEQ ID NO : 86

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1768	100.0	336	22	AAG80971	Human nGPCR54 #2.
2	1603.5	90.7	337	22	AAU04584	Human G-protein co
3	1602.5	90.6	337	22	AAU04375	Human G-protein co
4	1602.5	90.6	337	23	AAO15399	Human G protein-co
5	1602.5	90.6	337	23	ABB81902	Human G-protein co
6	1602.5	90.6	337	23	ABB83819	Human P2Y-like rec
7	1602.5	90.6	337	23	AAE21803	Human AXOR89 (G-pr
8	1602.5	90.6	337	23	ABB79438	Human P2Y1-li. Ho
9	1602.5	90.6	337	23	AAU77600	Human P2Y1-like G
10	1602.5	90.6	337	23	AAO14027	Human purinergic-r
11	1602.5	90.6	337	23	AAE16171	Human G-protein co
12	1275.5	72.1	276	23	ABB83818	Human P2Y-like rec
13	1098	62.1	230	22	AM79297	Human protein SEQ
14	997	56.4	192	22	AAG80958	Human nGPCR54 #1.
15	881.5	49.9	179	22	ABB11082	Human P2Y purinoce
16	881.5	49.9	179	22	AM80281	Human protein SEQ
17	525.5	29.7	373	22	AAE04389	Human P2-purinergi
18	525.5	29.7	373	23	AAU10983	Purinergic recepto
19	525.5	29.7	373	23	AAU10984	Purinergic re

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	525.5	29.7	373	2	JC4737	G protein-coupled
2	525	29.7	362	2	S33733	G protein-coupled
3	523.5	29.6	373	2	JC4162	P2Y receptor - bov
4	444.5	25.1	365	2	S68679	G protein-coupled
5	415	23.5	373	2	A47556	ATP receptor P2u -
6	414.5	23.4	420	2	I51667	thrombin receptor
7	390.5	22.1	375	2	A54946	P-2U nucleotide re
8	389.5	22.0	328	2	I55450	G protein-coupled
9	382	21.6	432	2	A43448	thrombin receptor
10	379	21.4	361	2	B45680	G protein-coupled
11	374.5	21.2	328	2	JC4800	P2Y6

RESULT 1

JC4737

G protein-coupled receptor P2Y1 - human

N;Alternate names: P2Y1 purinergic receptor; P2Y1 purinoceptor

C;Species: Homo sapiens (man)

C;Date: 10-May-1996 #sequence_revision 16-Aug-1996 #text_change 17-Nov-2000

C;Accession: JC4737; JC4615; S54253

R;Janssens, R.; Communi, D.; Piroton, S.; Samson, M.; Parmentier, M.; Boeynaems, J.M.

Biochem. Biophys. Res. Commun. 221, 588-593, 1996

A;Title: Cloning and tissue distribution of the human P2Y1 receptor.

A;Reference number: JC4737; MUID:96205320; PMID:8630005

A;Accession: JC4737

A;Molecule type: DNA

A;Residues: 1-373 <JAN>

A;Cross-references: GB:S81950; NID:g1839438; PIDN:AAB47091.1; PID:g1839439

R;Ayyanathan, K.; Webbbs, T.E.; Sandhu, A.K.; Athwal, R.S.; Barnard, E.A.; Kunapuli, S.P.

Biochem. Biophys. Res. Commun. 218, 783-788, 1996

A;Title: Cloning and chromosomal localization of the human P2Y1 purinoceptor.

A;Reference number: JC4615; MUID:96158962; PMID:8579591

A;Accession: JC4615

A;Molecule type: mRNA

A;Residues: 1-373 <AYY>

A;Cross-references: GB:U42029; NID:g1147730; PIDN:AAA97872.1; PID:g1147731

A;Experimental source: erythro leukemia cells
 R;Leon, C.; Vial, C.; Cazenave, J.; Gachet, C.
 submitted to the EMBL Data Library, May 1995
 A;Description: Cloning of a human putative P2Y receptor.
 A;Reference number: S54253
 A;Accession: S54253
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-137,139-373 <LEO>
 A;Cross-references: EMBL:Z49205; NID:g798835; PIDN:CAA89066.1; PID:g798836
 C;Comment: This receptor belongs to a family of G protein-coupled receptors. It responds
 to both ADP and ATP, and has several serine/threonine phosphorylation residues in the
 carboxyl terminus.
 C;Genetics:
 A;Gene: p2Y1; GDB:P2RY1
 A;Cross-references: GDB:677125; OMIM:601167
 A;Map position: 3pter-3qter
 C;Superfamily: ATP receptor P2u
 C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane
 protein
 F;52-77/Domain: transmembrane #status predicted <TM1>
 F;88-111/Domain: transmembrane #status predicted <TM2>
 F;124-152/Domain: transmembrane #status predicted <TM3>
 F;171-191/Domain: transmembrane #status predicted <TM4>
 F;214-237/Domain: transmembrane #status predicted <TM5>
 F;261-282/Domain: transmembrane #status predicted <TM6>
 F;305-328/Domain: transmembrane #status predicted <TM7>
 F;11,27,113,197/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;258,336/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status
 predicted
 F;330,339/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status
 predicted
 F;343/Binding site: phosphate (Ser) (covalent) (by protein kinase C and calmodulin-
 dependent kinase) #status predicted

Query Match 29.7%; Score 525.5; DB 2; Length 373;
 Best Local Similarity 34.5%; Pred. No. 1e-37;
 Matches 106; Conservative 64; Mismatches 118; Indels 19; Gaps 3;

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Qy      24 CTDENIPLKMHYLPVIYGIIFLVGFPGNAVISTYIFKMRPWKSSTIIMLNACTDLLYL 83
      |      : ||| : | ::||| ||| | | :| ||| :| :| ||| | ||:
Db      42 CALTKTGFQFYILPAVYILVFIIGFLGNSVAIWMFVHMKPWSGISVYMFNLALADFLYV 101

Qy      84 TSLPFLIHYYASGENWIFGDFMCKFIRFSFHFNLYSSILFLTCSIFRYCVIIHPMSCFS 143
      :|| || || : :||| ||| || || ||| ||||| || || :||:
Db     102 LTLPALIFYFNKTDWIFGDAMCKLQRFIFHVNLVGSILFLTCISAHRYSGVYVPLKSLG 161

Qy     144 IHKTRCAVVACAVVWIIISLVAVIPMTFLITSTNRTNRS-ACLDLTSSDELNTIKWYNLIL 202
      | : | : ||| : ||| : | :| : | || : | : | :| :
Db     162 RLKKNAICISVLVWLIVVVAISPILFYSGTGVKNTITCYDTSDEYLRSYFIYSMCT 221

Qy     203 TASTFCLPLVIVTLCYTTIIHTLTHGLQTDSCCLKQKARRLTILLLLAFYVCFLPPHILRV 262
      | : ||| ||| : || : | : ||| : | ||| : | :||| :| :
Db     222 TVAMFCVPLVLILGCYGLIVRALIYKDLDNSPLRRKSIYLVIIIVLTVFAVSYPFHVMKT 281

Qy     263 IQDRISACFQSVVPLRIRSMKLTSLFDH-----YAAINTFGNLLLYVVVSDNFQQ 312
      : | | ||| : :| | | :||| : :|| : | ||:
Db     282 MNLRARLDFQTPA-----MCAFNDRVYATYQVTRGLASLNSCVDPILYFLAGDTFRR 333

Qy     313 AVCSTVR 319
      : |
Db     334 RLSRATR 340
  
```

RESULT 2
 S33733
 G protein-coupled receptor - chicken
 C;Species: Gallus gallus (chicken)
 C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 24-Sep-1999

C;Accession: S33733
 R;Webb, T.E.; Simon, J.; Krishek, B.J.; Bateson, A.N.; Smart, T.G.; King, B.F.;
 Burnstock, G.; Barnard, E.A.
 FEBS Lett. 324, 219-225, 1993
 A;Title: Cloning and functional expression of a brain G-protein-coupled ATP receptor.
 A;Reference number: S33733; MUID:93285340; PMID:8508924
 A;Accession: S33733
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-362 <WEB>
 A;Cross-references: EMBL:X73268; NID:g395084; PIDN:CAA51716.1; PID:g395085
 C;Superfamily: ATP receptor P2u
 C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 29.7%; Score 525; DB 2; Length 362;
 Best Local Similarity 33.5%; Pred. No. 1.1e-37;
 Matches 113; Conservative 62; Mismatches 136; Indels 26; Gaps 5;

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Qy      1 MNEPLDYLANASDFPDYAA---AFGN----CTDENIPLKMHYLPVIYGIIFLVGFPGNAV 53
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1 MTEALISAALNGTQPELLAGGWAAGNATTKCSLTKTGFQFYLLPTVYILVFITGFLGNSV 60

Qy     54 VISTYIFKMRPWKSSTIIMLNLA CTDL LYL TSLPFLIHY YASGENWIFGDFMCKFIRFSF 113
      | :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     61 AIWMFVFHMRPWSGISVYMFNLALADFLYVLTLPALIFYFYNKTDWIFGDMCKLQRFIF 120

Qy    114 HFNLYSSILFLTCSIFRYCVIIHPMSCFSIHKTRCAVVACAVVWIIISLVAVIPMTFLI- 172
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    121 HVNLYGSILFLTCSISVHRYTG VVHPLKSLGR LKKKNVYVSSLVWALVVAVIAPILFYSG 180

Qy    173 TSTNRTNRSACDLTSSDELNTIKWYNLILTASTFCLPLVIVITLCYTTIIHTLTHGLQTD 232
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    181 TGVRNKITITCYDTTAD EYLRSYFVYSMCTTVFMFCIPFIVILGCYGLIVKALIYKDLDN 240

Qy    233 SCLKQKARRLTILLLLAFYVCF LPPFHILRVIQDRISACFQSVVPLRIRSMKLT SFLDH-- 290
      | :| :| :| | :| | | | | | | | | | | | | | | | | |
Db    241 SPLRRKSIYLVII VLT VFAVS YLPFHV MKTLNLRARLDFQ-----TPQMCAFN DKVY 292

Qy    291 -----YAALNTFGNLLLYVVSDNFQQA VCSTVR 319
      | :| | : :| | : | | : : |
Db    293 ATYQVTRGLASLNSCVDPILYFLAGDTFRRRLSRATR 329
  
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RESULT 3

JC4162
 P2Y receptor - bovine
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 12-Oct-1995 #sequence_revision 10-Nov-1995 #text_change 24-Sep-1999
 C;Accession: JC4162
 R;Henderson, D.J.; Elliot, D.G.; Smith, G.M.; Webb, T.E.; Dainty, I.A.
 Biochem. Biophys. Res. Commun. 212, 648-656, 1995
 A;Title: Cloning and characterisation of a bovine P2Y receptor.
 A;Reference number: JC4162; MUID:95352058; PMID:7626079
 A;Accession: JC4162
 A;Molecule type: mRNA
 A;Residues: 1-373 <HEN>
 A;Cross-references: EMBL:X87628; NID:g1032484; PIDN:CAA60958.1; PID:g1032485
 A;Experimental source: aortic endothelial cell
 C;Genetics:
 A;Gene: bovp2y
 C;Superfamily: ATP receptor P2u
 C;Keywords: glycoprotein; phosphoprotein; receptor; transmembrane protein
 F;52-77/Domain: transmembrane #status predicted <TM1>
 F;88-111/Domain: transmembrane #status predicted <TM2>
 F;124-150/Domain: transmembrane #status predicted <TM3>
 F;171-191/Domain: transmembrane #status predicted <TM4>
 F;214-237/Domain: transmembrane #status predicted <TM5>
 F;261-282/Domain: transmembrane #status predicted <TM6>
 F;305-328/Domain: transmembrane #status predicted <TM7>

F;11,27,113,197/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;258/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted

Query Match 29.6%; Score 523.5; DB 2; Length 373;
Best Local Similarity 34.5%; Pred. No. 1.5e-37;
Matches 106; Conservative 64; Mismatches 118; Indels 19; Gaps 3;

```

Qy      24 CTDENIPLKMHYLPVIYGIIFLVGFPGNAVVISITYIFKMRPWKSSTIIMLNACTDLLYL 83
      |      : : || : : : : || : : | : || : : | ||| | ||:
Db      42 CALTKTGFQFYLLPAVYILVFIIGFLGNSVAIWMFVFMKPKWSGISVYMFNLALADFLYV 101

Qy      84 TSLPFLIHYYASGENWIFGDFMCKFIRFSFHFNLYSSILFLTCSIFRYCVIIHPMSCFS 143
      : || || | : : |||| | | | | | | | | | | | | | : : : :
Db      102 LTLPALIFYFYFNKTDWIFGDAMCKLQRFIFHVNLYGSILFLTCSIAHRYSGVVYPLKSLG 161

Qy      144 IHKTRCAVAVACAVVWIIISLVAVIPMTFLITSTNRNRS-ACLDLTSSDELNTIKWYNLIL 202
      | : || : || : : | : : | : : | || : | : | : :
Db      162 RLKKKNNAVYISVLVWLVVVGISPILFYSYSGTGIRKNKNTITCYDTSDEYLRSYFIYSMCT 221

Qy      203 TASTFCLPLVIVTLCYTTIIHTLTHGLQTDSCCLKQKARRLTILLLLAFYVCFLPFHILRV 262
      | : ||: || : : | : : | : : | : : | | : : || : : :
Db      222 TVAMFCVPLVLILGCGYLIVRALIYKDLDNSPLRRKSIYLVIIIVLTVFAVSYPFHVMKT 281

Qy      263 IQDRISACFQSVVPLRIRSMKLTSLFDH-----YAALNTFGNLLLVVVSDNFQQ 312
      : |      ||      : : : |      | : || : : : | : | : :
Db      282 MNLRLARLDQF-----TPEMCAFNDRVYATYQVTRGLASLNSCVDPILYFLAGDTFRR 333

Qy      313 AVCSTVR 319
      :      |
Db      334 RLSRATR 340

```

RESULT 5

A47556

ATP receptor P2u - mouse

C;Species: Mus musculus (house mouse)

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-Sep-1999

C;Accession: A47556

R; Lustig, K.D.; Shiau, A.K.; Brake, A.J.; Julius, D.

Proc. Natl. Acad. Sci. U.S.A. 90, 5113-5117, 1993

A;Title: Expression cloning of an ATP receptor from mouse neuroblastoma cells.

A;Reference number: A47556; MUID:93281707; PMID:7685114

A;Accession: A47556

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-373 <LUS>

A;Cross-references: GB:L14751; NID:g309457; PIDN:AAA39871.1; PID:g309458

C;Superfamily: ATP receptor P2u

Query Match 23.5%; Score 415; DB 2; Length 373;
Best Local Similarity 33.7%; Pred. No. 3.2e-28;
Matches 82; Conservative 50; Mismatches 101; Indels 10; Gaps 2;

Qy	28	NIPLKMHYLPVIYGIIFLVGFPGNAAVVISTYIFKMRPWKSSTIIMLNLA C TDLLYLTSLP	87
		: : : : : : : :	
Db	28	NEDFKYVLLPVSYGVVCVLGLCLNVVALYIFLCRLKTWNASTTYMFHLAVSDSLYAASLP	87
Qy	88	FLIHYYASGENWIFGDFMCKFIRFSFHFNLYSSILFLTCSIFRYCVIIHPMSCFSIHKT	147
		: : : : : : : : : : :	
Db	88	LLVYYYARGDHWPFSTVLCKLVRFLFYTNLYCSILFLTCSIVHRCGLVLRPLHSLRWGRA	147
Qy	148	RCAVVACAVVWIISLVAVIPMTFLTITSTNRTNRSACLDTSSDELNTIKWYNLILTASTF	207
		: : : : : : : : : : : : :	
Db	148	RYARRVAADVWLVLACQAPVLYFVTTSVRGRITRCHDTSARELFSHFVAYSSVMLGLLF	207
Qy	208	CLPLVIVTLCYTTHIHTL-----THGLQTDSCLKQKARRLTILLLLAFYVCFLPFIL	260
		: : : : : : : : : : : : :	
Db	208	AVPFVSILVCYVLMARRLLKPAYGTGGGLPR--AKRRSVRTIALVLAVFALCFLPFPHVT	264

Qy	261	RVI	263
		:	
Db	265	RTL	267